

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/686,490C
Source: IFWO
Date Processed by STIC: 2/25/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>10/686,490C</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <u> </u> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <u> </u> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <u> </u> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <u> </u> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <u> </u> Variable Length	Sequence(s) <u> </u> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <u> </u> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <u> </u> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <u> </u> Skipped Sequences (OLD RULES)	Sequence(s) <u> </u> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO: X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <u> </u> Skipped Sequences (NEW RULES)	Sequence(s) <u> </u> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <u> </u> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <u> </u> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <u> </u> Use of <220>	Sequence(s) <u> </u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <u> </u> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <u> </u> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

RAW SEQUENCE LISTING

DATE: 02/25/2005

PATENT APPLICATION: US/10/686,490C

TIME: 10:06:06

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\02252005\J686490C.raw

3 <110> APPLICANT: Bayer Aktiengesellschaft
 4 <120> TITLE OF INVENTION: Anti-Kazlauskas-Lipases
 5 <130> FILE REFERENCE: LeA 35 991
 C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/686,490C
 C--> 6 <141> CURRENT FILING DATE: 2003-10-15
 6 <160> NUMBER OF SEQ ID NOS: 2
 7 <170> SOFTWARE: PatentIn version 3.1
 9 <210> SEQ ID NO: 1
 10 <211> LENGTH: 885
 11 <212> TYPE: DNA
 12 <213> ORGANISM: unknown
 13 <220> FEATURE:
 14 <221> NAME/KEY: CDS
 15 <222> LOCATION: (1)..(885)
 16 <223> OTHER INFORMATION: bacterial
 18 <400> SEQUENCE: 1
 19 atg gca cag gtg aag gcc aac ggc att acc ctg gag tat gaa gag cag 48
 20 Met Ala Gln Val Lys Ala Asn Gly Ile Thr Leu Glu Tyr Glu Glu Gln
 21 1 5 10 15
 23 ggc cat cgc cac cat ccg tcc atg ctg ctg att atg ggc ctg ggc ggc 96
 24 Gly His Arg His His Pro Ser Met Leu Leu Ile Met Gly Leu Gly Gly
 25 20 25 30
 27 cag tta atc gac tgg ccc gag gag ttc atc cgg ggg ctg gct gaa cga 144
 28 Gln Leu Ile Asp Trp Pro Glu Glu Phe Ile Arg Gly Leu Ala Glu Arg
 29 35 40 45
 31 ggc ttc cgg gta atc tgt ttc gac aac cgc gac ggc ggg ctt tcg acg 192
 32 Gly Phe Arg Val Ile Cys Phe Asp Asn Arg Asp Ala Gly Leu Ser Thr
 33 50 55 60
 35 aaa ctt gaa ggc gtg aaa aaa ccg aac att gcc cgg gta ttt ctg ctg 240
 36 Lys Leu Glu Gly Val Lys Lys Pro Asn Ile Ala Arg Val Phe Leu Leu
 37 65 70 75 80
 39 gcg agc atg ggc cta aag ccc agg gtg cct tac acc ctg gac gac atg 288
 40 Ala Ser Met Gly Leu Lys Pro Arg Val Pro Tyr Thr Leu Asp Asp Met
 41 85 90 95
 43 gcc ctg gac acc gtg ggg ctg atg gat gcc ctg ggc att gag agc acc 336
 44 Ala Leu Asp Thr Val Gly Leu Met Asp Ala Leu Gly Ile Glu Ser Thr
 45 100 105 110
 47 cac gta gtt ggc gtc tcc atg ggc ggc atg att gcg cag att cta ggg 384
 48 His Val Val Gly Val Ser Met Gly Gly Met Ile Ala Gln Ile Leu Gly
 49 115 120 125
 51 gcg aag cac ggg gag cgg gtg aaa tcc ctt acc ctg atg att acc tcc 432
 52 Ala Lys His Gly Glu Arg Val Lys Ser Leu Thr Leu Met Ile Thr Ser
 53 130 135 140

*see item 4 on Euro
 Summary Sheet*

pp 2,4

**Does Not Comply
 Corrected Diskette Needed**

RAW SEQUENCE LISTING

DATE: 02/25/2005

PATENT APPLICATION: US/10/686,490C

TIME: 10:06:06

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\02252005\J686490C.raw

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55 tcc ggc aac ccc cgc atg ccg gcg ccc agg ccg cag gtg ctg caa aag      480
56 Ser Gly Asn Pro Arg Met Pro Ala Pro Arg Pro Gln Val Leu Gln Lys
57 145                      150                      155                      160
59 ttt atg cgg gtg ccc aag agc atg gat aag gaa gag tgg att aaa tac      528
60 Phe Met Arg Val Pro Lys Ser Met Asp Lys Glu Glu Trp Ile Lys Tyr
61                      165                      170                      175
63 aac ttg gag ctt tta acc acc atc ggc agc ccc ggg ttg gac cgg gag      576
64 Asn Leu Glu Leu Leu Thr Thr Ile Gly Ser Pro Gly Leu Asp Arg Glu
65                      180                      185                      190
67 aag ctg gcc tta gac gtg agg aag agc ata gag cgg tgc ctt tgc ccc      624
68 Lys Leu Ala Leu Asp Val Arg Lys Ser Ile Glu Arg Cys Leu Cys Pro
69                      195                      200                      205
71 gaa ggc acg cag cgg cag ctg gca gcc atc ctg cag agc ggc agc agg      672
72 Glu Gly Thr Gln Arg Gln Leu Ala Ala Ile Leu Gln Ser Gly Ser Arg
73                      210                      215                      220
75 gtg aag ctg ctc cgg cgg atc gct gtc ccc acc ctg gtc atc agc ggg      720
76 Val Lys Leu Leu Arg Arg Ile Ala Val Pro Thr Leu Val Ile Ser Gly
77 225                      230                      235                      240
79 gcg gaa gat ccc ctc ctg ccg tac cag tgc ggc cgg gac att gcc gac      768
80 Ala Glu Asp Pro Leu Leu Pro Tyr Gln Cys Gly Arg Asp Ile Ala Asp
81                      245                      250                      255
83 cat atc ccg gga gcc cgc ttc gag ctc atc gag ggc atg ggg cac gac      816
84 His Ile Pro Gly Ala Arg Phe Glu Leu Ile Glu Gly Met Gly His Asp
85                      260                      265                      270
87 att ccc gag cgg cac atc ccc cgg ctg att gag ctc atc gcc ggg cac      864
88 Ile Pro Glu Arg His Ile Pro Arg Leu Ile Glu Leu Ile Ala Gly His
89                      275                      280                      285
91 gcc gcg gcc gcg gaa gct taa      885
92 Ala Ala Ala Ala Glu Ala
93                      290

```

96 <210> SEQ ID NO: 2

97 <211> LENGTH: 294

98 <212> TYPE: PRT

99 <213> ORGANISM: unknown

W--> 102 <220> FEATURE:

W--> 102 <223> OTHER INFORMATION:

W--> 102 <400> 2

```

104 Met Ala Gln Val Lys Ala Asn Gly Ile Thr Leu Glu Tyr Glu Glu Gln
105 1                      5                      10                      15
108 Gly His Arg His His Pro Ser Met Leu Leu Ile Met Gly Leu Gly Gly
109                      20                      25                      30
112 Gln Leu Ile Asp Trp Pro Glu Glu Phe Ile Arg Gly Leu Ala Glu Arg
113                      35                      40                      45
116 Gly Phe Arg Val Ile Cys Phe Asp Asn Arg Asp Ala Gly Leu Ser Thr
117                      50                      55                      60
120 Lys Leu Glu Gly Val Lys Lys Pro Asn Ile Ala Arg Val Phe Leu Leu
121 65                      70                      75                      80
124 Ala Ser Met Gly Leu Lys Pro Arg Val Pro Tyr Thr Leu Asp Asp Met
125                      85                      90                      95

```

see p. 4 for error explanation

RAW SEQUENCE LISTING

DATE: 02/25/2005

PATENT APPLICATION: US/10/686,490C

TIME: 10:06:06

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\02252005\J686490C.raw

```

128 Ala Leu Asp Thr Val Gly Leu Met Asp Ala Leu Gly Ile Glu Ser Thr
129      100      105      110
132 His Val Val Gly Val Ser Met Gly Gly Met Ile Ala Gln Ile Leu Gly
133      115      120      125
136 Ala Lys His Gly Glu Arg Val Lys Ser Leu Thr Leu Met Ile Thr Ser
137      130      135      140
140 Ser Gly Asn Pro Arg Met Pro Ala Pro Arg Pro Gln Val Leu Gln Lys
141 145      150      155      160
144 Phe Met Arg Val Pro Lys Ser Met Asp Lys Glu Glu Trp Ile Lys Tyr
145      165      170      175
148 Asn Leu Glu Leu Leu Thr Thr Ile Gly Ser Pro Gly Leu Asp Arg Glu
149      180      185      190
152 Lys Leu Ala Leu Asp Val Arg Lys Ser Ile Glu Arg Cys Leu Cys Pro
153      195      200      205
156 Glu Gly Thr Gln Arg Gln Leu Ala Ala Ile Leu Gln Ser Gly Ser Arg
157      210      215      220
160 Val Lys Leu Leu Arg Arg Ile Ala Val Pro Thr Leu Val Ile Ser Gly
161 225      230      235      240
164 Ala Glu Asp Pro Leu Leu Pro Tyr Gln Cys Gly Arg Asp Ile Ala Asp
165      245      250      255
168 His Ile Pro Gly Ala Arg Phe Glu Leu Ile Glu Gly Met Gly His Asp
169      260      265      270
172 Ile Pro Glu Arg His Ile Pro Arg Leu Ile Glu Leu Ile Ala Gly His
173      275      280      285
176 Ala Ala Ala Ala Glu Ala
177      290

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/686,490C

DATE: 02/25/2005
TIME: 10:06:07

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\02252005\J686490C.raw

error explanation
Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:2

VERIFICATION SUMMARY

DATE: 02/25/2005

PATENT APPLICATION: US/10/686,490C

TIME: 10:06:07

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\02252005\J686490C.raw

L:6 M:270 C: Current Application Number differs, Replaced Current Application No

L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:102 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
ORGANISM:unknownL:102 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:unknown

L:102 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:102